Development of SNPs markers (Single Nucleotide Polymorphisms) presents in regulatory regions and genotyping of mapping population *Hevea brasiliensis*

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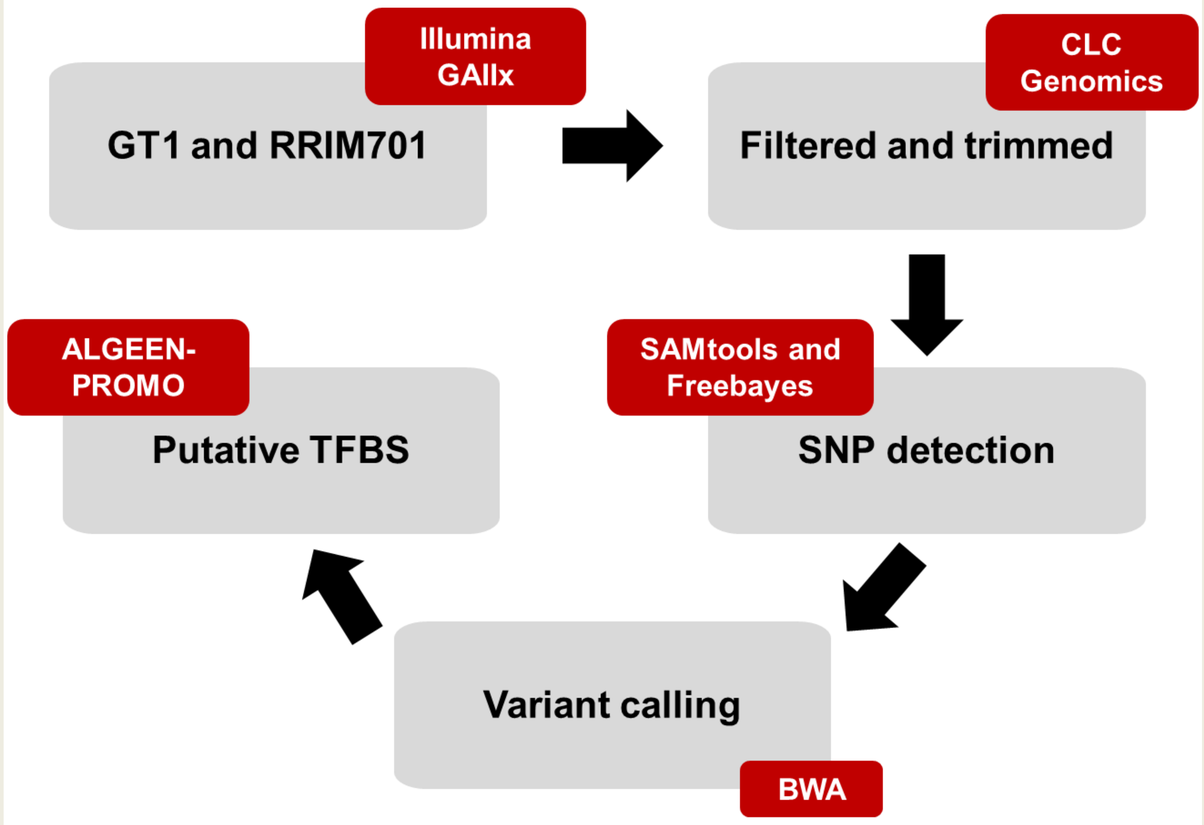
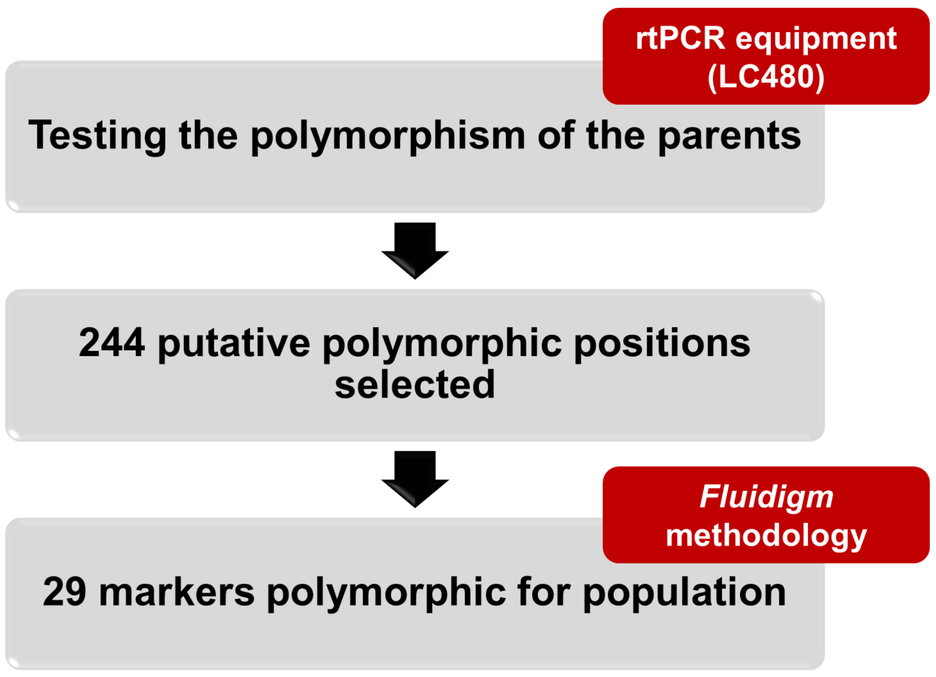
INTRODUCTION

The rubber tree (Hevea spp.), primary plant used for natural rubber production, have a long breeding cycle. However, the advent of molecular genetic markers favored early assessment methods, allowing the characterization of genotypes, genetic diversity analysis, QTL analysis and identifying genes of interest. This project aims to develop and genotype new SNP markers presents/or near in putative transcription factor binding sites (TFBS) to two genetic mapping populations of rubber tree obtained from the crossing between RRIM701xGT1 and PB235xGT1 clones.

MATERIAL AND METHODS



❖ Identification of SNP allelic: KASPAR chemistry

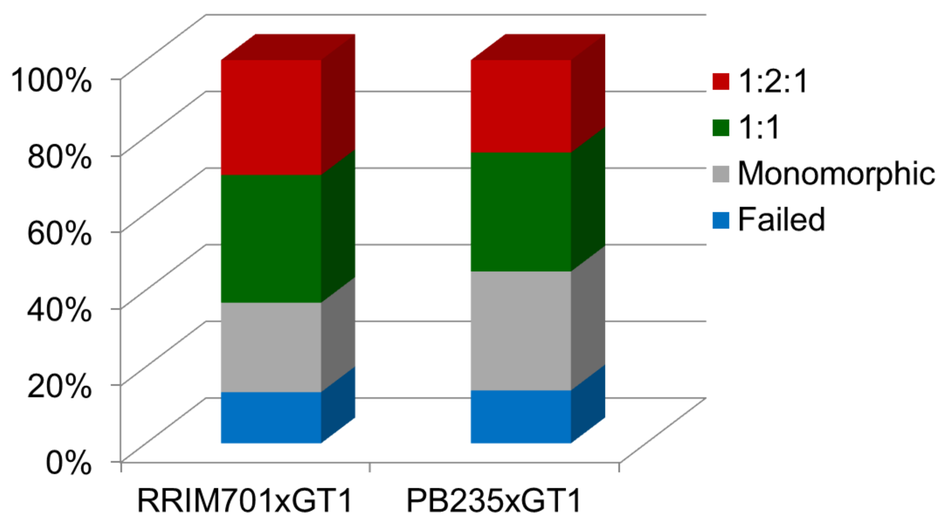


RESULTS AND DISCUSSION

❖ Freebayes detected 59,267 putative SNPs: 39,455 transitions (ts) and 19,812 transversions (tv) → Ts/Tv=1,99

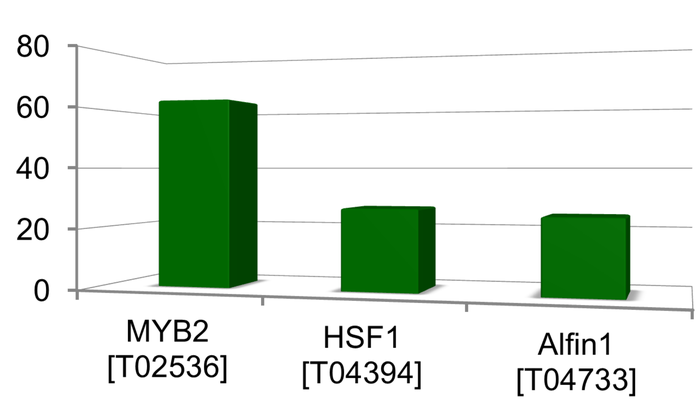
❖ Were identified 19,118 polymorphic positions in the GT1 and 25,360 polymorphic positions in the RRIM701, of which a total of 14,568 putative SNPs was shared between cultivars.

Segregation obtained from the genotyping of two population according Wu et al. (2002)



❖ 27 putative TFBS different were found by the program ALGGEN-PROMO, where highlight MYB2, HSF1 and Alfin1 as the most frequent, respectively (figure below).

Putative Transcription Factor Binding Sites Annotated



CONCLUSION

The transcription factors are involved in the response to biotic and abiotic stresses and your study allow increase knowledge of the mesh of responses that plants use to defend environmental stresses. The results show SNP markers presents/or near in putative transcription factor binding sites (TFBS) genotiped with success in two populations of mapping.

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